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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
- (ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 45
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/231,565
(B) FILING DATE: 22-APR-1994
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CAROL M. GRUPPI
(B) REGISTRATION NUMBER: 37,341
(C) REFERENCE/DOCKET NUMBER: 2026-4124
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1559
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGACAGA	GGACTCTCAT	TAAGGAAGGT	GTCCTGTGCC	40
CTGACCCTAC	AAGATGCCAA	GAGAAGATGC	TCACTTCATC	80
TATGGTTACC	CCAAGAAGGG	GCACGGCCAC	TCTTACACCA	120
CGGCTGAAGA	GGCCGCTGGG	ATCGGCATCC	TGACAGTGAT	160
CCTGGGAGTC	TTACTGCTCA	TCGGCTGTTG	GTATTGTAGA	200
AGACGAAATG	GATACAGAGC	CTTGATGGAT	AAAAGTCTTC	240
ATGTTGGCAC	TCAATGTGCC	TTAACAAGAA	GATGCCCACA	280
AGAAGGGTTT	GATCATCGGG	ACAGCAAAGT	GTCTCTTCAA	320
GAGAAAACT	GTGAACCTGT	GGTTCCCAAT	GCTCCACCTG	360
CTTATGAGAA	ACTCTCTGCA	GAACAGTCAC	CACCACCTTA	400
TTCACCTTAA	GAGCCAGCGA	GACACCTGAG	ACATGCTGAA	440
ATTATTTCTC	TCACACTTTT	GCTTGAATTT	AATACAGACA	480
TCTAATGTTT	TCCTTTGGAA	TGGTGTAGGA	AAAATGCAAG	520
CCATCTCTAA	TAATAAGTCA	GTGTTAAAAT	TTTAGTAGGT	560
CCGCTAGCAG	TACTAATCAT	GTGAGGAAAT	GATGAGAAAT	600
ATTAAATTGG	GAAAACTCCA	TCAATAAATG	TTGCAATGCA	640
TGATACTATC	TGTGCCAGAG	GTAATGTTAG	TAAATCCATG	680
GTGTTATTTT	CTGAGAGACA	GAATTCAAGT	GGGTATTCTG	720
GGGCCATCCA	ATTCTCTTTT	ACTTGAAATT	TGGCTAATAA	760
CAAAC TAGTC	AGGTTTTTCGA	ACCTTGACCG	ACATGAACTG	800
TACACAGAAT	TGTTC CAGTA	CTATGGAGTG	CTCACAAAGG	840
ATACTTTTAC	AGGTTAAGAC	AAAGGGTTGA	CTGGCCTATT	880
TATCTGATCA	AGAACATGTC	AGCAATGTCT	CTTTGTGCTC	920
TAAAATTCTA	TTATACTACA	ATAATATATT	GTAAAGATCC	960
TATAGCTCTT	TTTTTTTGAG	ATGGAGTTTC	GCTTTTGTTG	1000
CCCAGGCTGG	AGTGCAATGG	CGCGATCTTG	GCTCACCATA	1040
ACCTCCGCCT	CCCAGGTTCA	AGCAATTCTC	CTGCCTTAGC	1080

CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC 1120
 TGACTAATTT TGTAGTTTTA GTAGAGACGG GGTTCCTCCA 1160
 TGTGAGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT 1200
 CTGCCCCGCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG 1240
 TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG 1280
 ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA 1320
 ATGCTATTCT AACTAATGAC AAGTATTTTC TACTAAACCA 1360
 GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG 1400
 TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT 1440
 ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC 1480
 TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT 1520
 TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1559

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys
 1 5 10
 Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala
 15 20 25
 Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu
 30 35 40
 Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
 45 50 55
 Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu
 60 65 70

Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
75 80
Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
85 90 95
Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110
Pro Pro Pro Tyr Ser Pro
115

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown
(ii) MOLECULE TYPE: Peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown
(ii) MOLECULE TYPE: Peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Ile Gly Ile Leu Thr Val Ile Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Leu Thr Val Ile Leu Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Leu Thr Val Ile Leu Gly Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Val Ile Leu Gly Val Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Ile Leu Gly Val Leu Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Ile Leu Gly Val Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Leu Met Asp Lys Ser Leu His Val
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu His Val Gly Thr Gln Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Val Val Pro Asn Ala Pro Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ala Pro Pro Ala Tyr Glu Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid

(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Ile Leu Thr Val Ile Leu Gly Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Leu Thr Val Ile Leu Gly Val Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Val Ile Leu Gly Val Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Val Ile Leu Gly Val Leu Leu Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Ala Leu Met Asp Lys Ser Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Leu His Val Gly Thr Gln Cys Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2172
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40
 GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80
 ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120
 GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160
 CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200
 GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240
 TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280
 TGCCTCCTTC TCTATTGCCT TGAACITCCC TGAAGCCAA 320
 AAGGTATTGC CAGATGGGCA GGTATCTGG GTCAACAATA 360
 CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520
ATTTCTAGGG GGCCCACTGT CTGGGCTGAG CATTGGGACA 560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGA CTG 600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC 760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920
GCCATTCCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCTAA 1000
CACCACAGCT GGCCAAGTGC CTA CTACTACAGA AGTTGTGGGT 1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120
TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA 1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480

TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA 1520
 AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560
 ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC 1600
 CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640
 CCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680
 CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG 1720
 CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760
 AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800
 GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840
 CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880
 ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920
 CCCAGTTGCC ACATAGCAGC AGTCACTGGC TCGTCTACC 1960
 CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC 2000
 CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040
 CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080
 CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT 2120
 ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160
 AAAAAAAAAA AA 2172

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu
 1 5 10

Ala	Val	Ile	Gly	Ala	Leu	Leu	Ala	Val	Gly	Ala	Thr
		15					20				
Lys	Val	Pro	Arg	Asn	Gln	Asp	Trp	Leu	Gly	Val	Ser
25					30					35	
Arg	Gln	Leu	Arg	Thr	Lys	Ala	Trp	Asn	Arg	Gln	Leu
			40					45			
Tyr	Pro	Glu	Trp	Thr	Glu	Ala	Gln	Arg	Leu	Asp	Cys
	50					55				60	
Trp	Arg	Gly	Gly	Gln	Val	Ser	Leu	Lys	Val	Ser	Asn
				65					70		
Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala	Asn	Ala	Ser	Phe
		75					80				
Ser	Ile	Ala	Leu	Asn	Phe	Pro	Gly	Ser	Gln	Lys	Val
85					90					95	
Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Val	Asn	Asn	Thr
			100					105			
Ile	Ile	Asn	Gly	Ser	Gln	Val	Trp	Gly	Gly	Gln	Pro
	110					115					120
Val	Tyr	Pro	Gln	Glu	Thr	Asp	Asp	Ala	Cys	Ile	Phe
				125					130		
Pro	Asp	Gly	Gly	Pro	Cys	Pro	Ser	Gly	Ser	Trp	Ser
		135					140				
Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp
145					150					155	
Gly	Gln	Tyr	Trp	Gln	Phe	Leu	Gly	Gly	Pro	Val	Ser
			160					165			
Gly	Leu	Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly
	170					175					180
Thr	His	Thr	Met	Glu	Val	Thr	Val	Tyr	His	Arg	Arg
				185					190		
Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	Ser	Ser
		195					200				
Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser
205					210					215	
Val	Ser	Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly
			220					225			
Asn	Lys	His	Phe	Leu	Arg	Asn	Gln	Pro	Leu	Thr	Phe
	230					235					240
Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala
				245					250		
Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp
		255					260				
Ser	Ser	Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val
260					265					270	
Thr	His	Thr	Tyr	Leu	Glu	Pro	Gly	Pro	Val	Thr	Ala
			275						280		
Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser
	285					290					295
Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly
				300					305		
His	Arg	Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala
		310					315				
Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Val	Gly	Thr	Thr
320					325					330	

A
B'

Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	Gly	Thr
			335					340			
Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser
	345					350					355
Thr	Ala	Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr
				360					365		
Gly	Met	Thr	Pro	Glu	Lys	Val	Pro	Val	Ser	Glu	Val
		370					375				
Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	Pro	Glu
380					385					390	
Ala	Thr	Gly	Met	Thr	Pro	Ala	Glu	Val	Ser	Ile	Val
			395					400			
Val	Leu	Ser	Gly	Thr	Thr	Ala	Ala	Gln	Val	Thr	Thr
	405					410					415
Thr	Glu	Trp	Val	Glu	Thr	Thr	Ala	Arg	Glu	Leu	Pro
				420					425		
Ile	Pro	Glu	Pro	Glu	Gly	Pro	Asp	Ala	Ser	Ser	Ile
		430					435				
Met	Ser	Thr	Glu	Ser	Ile	Thr	Gly	Ser	Leu	Gly	Pro
440					445					450	
Leu	Leu	Asp	Gly	Thr	Ala	Thr	Leu	Arg	Leu	Val	Lys
			455					460			
Arg	Gln	Val	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg	Tyr
	465				470						475
Gly	Ser	Phe	Ser	Val	Thr	Leu	Asp	Ile	Val	Gln	Gly
				480					490		
Ile	Glu	Ser	Ala	Glu	Ile	Leu	Gln	Ala	Val	Pro	Ser
		495					500				
Gly	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr	Val	Ser	Cys
505					510					515	
Gln	Gly	Gly	Leu	Pro	Lys	Glu	Ala	Cys	Met	Glu	Ile
			520					525			
Ser	Ser	Pro	Gly	Cys	Gln	Pro	Pro	Ala	Gln	Arg	Leu
	530					535					540
Cys	Gln	Pro	Val	Leu	Pro	Ser	Pro	Ala	Cys	Gln	Leu
				545					550		
Val	Leu	His	Gln	Ile	Leu	Lys	Gly	Gly	Ser	Gly	Thr
		555					560				
Tyr	Cys	Leu	Asn	Val	Ser	Leu	Ala	Asp	Thr	Asn	Ser
565					570					575	
Leu	Ala	Val	Val	Ser	Thr	Gln	Leu	Ile	Met	Pro	Gly
			580					585			
Gln	Glu	Ala	Gly	Leu	Gly	Gln	Val	Pro	Leu	Ile	Val
	590					595					600
Gly	Ile	Leu	Leu	Val	Leu	Met	Ala	Val	Val	Leu	Ala
				605					610		
Ser	Leu	Ile	Tyr	Arg	Arg	Arg	Leu	Met	Lys	Gln	Asp
		615					620				
Phe	Ser	Val	Pro	Gln	Leu	Pro	His	Ser	Ser	Ser	His
625					630					635	
Trp	Leu	Arg	Leu	Pro	Arg	Ile	Phe	Cys	Ser	Cys	Pro
			640					645			
Ile	Gly	Glu	Asn	Ser	Pro	Leu	Leu	Ser	Gly	Gln	Gln
	650					655					660

A
B'

Val

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Val Gln Pro Val Pro Gly Ile Leu Leu Thr Leu
1 5 10
Leu Ser Gly Gln Gln Val
15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Val Gln Leu Val Pro Gly Ile Leu Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Val Gln Leu Val Pro Gly Ile Leu Leu Thr
1 5 10


```

(i)      SEQUENCE CHARACTERISTICS:
          (A)  LENGTH:  11
          (B)  TYPE:    amino acid
          (C)  STRANDEDNESS:  Unknown
          (D)  TOPOLOGY:  Unknown

(ii)     MOLECULE TYPE:  Protein

(xi)     SEQUENCE DESCRIPTION:  SEQ ID NO:31:

```

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11
 (B) TYPE: amino acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Leu Val Pro Gly Ile Leu Leu Thr Pro Pro Gln
1 5 10
Trp Ala Ala Gly Leu Ser Thr Leu Ile
15 20

(2) INFORMATION FOR SEQ ID NO:33:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
```

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Leu Asp Gly Gly Asn Lys His Phe Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Leu Lys Arg Cys Leu Leu His Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10  
(B) TYPE: amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Leu Pro Ser Pro Ala Cys Gln Leu Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Leu Ala Asp Thr Asn Ser Leu Ala Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Val Ser Val Ser Gln Leu Arg Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Tyr Leu Glu Pro Gly Pro Val Thr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Asn Val Ser Leu Ala Asp Thr Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58
- (B) TYPE: NUCLEOTIDE
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGACAGGCCG AGGCGGCCTT TTTTTTTTTT TTTTTTTTTT  
TTTTTTTTTT TTTTTTTT

40  
58

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: NUCLEOTIDE
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCAATCGCGA CC

12

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: NUCLEOTIDE
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTCGCGATTG GTAA

14

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9

(B) TYPE: amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5